SEQUENCE LISTING

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| <110> | Ecole Polytechnique Fédérale de Lausanne (EPFL) |
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| | Method for identification of suitable fragmentation sites in a reprotein |
| <130> | PEPF001WO |
| | US 34,404 JM-213 2003-10-09 |
| <160> | 66 |
| <170> | PatentIn version 3.1 |
| <210> | 1 |
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| <223> | silent point mutation introduced to generate $\ensuremath{HindIII}$ restriction site |
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| <309> | 2004-08-30 |

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Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile 35 40 45

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys 50 55 60 3

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln 65 70 75 80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile 85 90 95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu 100 105 110

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile 115 120 125

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe 130 135

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile 145 $$ 150 $$ 150 $$ 155 $$ 160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met 165 \$170\$

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu $180 \hspace{1.5cm} 185 \hspace{1.5cm} 190 \hspace{1.5cm}$

Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val Glu Thr Asn Gly 195 200

Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys 210 215 220

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| gttttggctc tggtcaatga ttacggcatt gatatcgtcc aactgcacgg agatgagtcg | 180 |
| tggcaagaat accaagagtt cctcggtttg ccagttatta aaagactcgt atttccaaaa | 240 |
| gactgcaaca tactactcag tgcagcttca cagaaacctc attcgtttat tcccttgttt | 300 |
| gattcagaag caggtgggac aggtgaactt ttggattgga | 360 |
| ggaaggcaag agagccccga gagcttacat tttatgttag ctggtggact gacgccagaa | 420 |
| aatgttggtg atgcgcttag attaaatggc gttattggtg ttgatgtaag cggaggtgtg | 480 |

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Lys Ala Tyr Lys Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val $20 \\ 25 \\ 30$

Phe Arg Asn Gln Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr \$35\$

Gly Ile Asp Ile Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr 50 55 60

Gln Glu Phe Leu Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys 65 70 75 80

Asp Cys Asn Ile Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe 85 90 95

Ile Pro Leu Phe Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110 \hspace{1.5cm}$

Trp Asn Ser Ile Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser 115 120 125

Leu His Phe Met Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp 130 \$135\$

Ala Leu Arg Leu Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val 145 $$ 150 $$ 155 $$ 160

Glu Thr Asn Gly Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val Lys 165 170 175

Asn Ala Lys Lys 180

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| gtgcccaata gaaagagaac aattgacccg gttattgca 159 |
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| coggooggog cycloogeda codacceday yayyacyccc cyyclocyyc Cddcydccdc 120 |

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ggtttgecag ttattaaaag actegtattt eeaaaagact geaaeatact acteagtgea 240
getteacaga aaceteatte gtttatteee ttgtttgatt eagaageagg tgggacaggt 300
gaacttttgg attggaacte gatttetgae tgggttggaa ggcaagagag eeeggagag 2360
ttacattta tgttagetgg tggactgaeg eeagaaaatg ttggtgatge gettagatta 420
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Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln Pro Lys Glu Asp 20 25 30

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Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu Gly Leu Pro Val 50 55 60

Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile Leu Leu Ser Ala 65 70 75 80

Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe Asp Ser Glu Ala 85 90 95

Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile Ser Asp Trp Val

Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met Leu Ala Gly Gly

Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu Asn Gly Val Ile 130 135 140 Gly Val Asp Val Ser Gly Gly Val Glu Thr Asn Gly Val Lys Asp Ser 145 150 155 Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys 165 <210> 11 <211> 561 <212> DNA <213> Saccharomyces cerevisiae <400> 11 atgtctgtta ttaatttcac aggtagttct ggtccattgg tgaaagtttg cggcttgcag 60 agcacagagg cogcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt 120 qtqcccaata qaaaqaqaac aattqacccq qttattqcaa qqaaaatttc aaqtcttqta 180 aaagettata aaaatagtte aggeacteeg aaataettgg ttggegtgtt tegtaateaa 240 cctaaggagg atgttttggc tctggtcaat gattacggca ttgatatcgt ccaactgcac 300 qqaqatqaqt cqtqqcaaqa ataccaaqaq ttcctcqqtt tqccaqttat taaaaqactc 360 qtatttccaa aaqactqcaa catactactc aqtqcaqctt cacaqaaacc tcattcqttt 420 attocottot ttoattoaga aggaggtggg agaggtgaac ttttggattg gaactogatt 480 tctgactggg ttggaaggca agagagcccc gagagcttac attttatgtt agctggtgga 540 ctgacgccag aaaatgttgg t 561 <210> 12 <211> 187 <212> PRT <213> Saccharomyces cerevisiae <400> 12 Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp 20 25 30

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| Asp | Pro 50 | Val | Ile | Ala | Arg | Lys 55 | Ile | Ser | Ser | Leu | Val 60 | Lys | Ala | Tyr | Lys |
| Asn 65 | Ser | Ser | Gly | Thr | Pro 70 | Lys | Tyr | Leu | Val | Gly 75 | Val | Phe | Arg | Asn | Gln 80 |
| Pro | Lys | Glu | Asp | Val 85 | Leu | Ala | Leu | Val | Asn 90 | Asp | Tyr | Gly | Ile | Asp 95 | Ile |
| Val | Gln | Leu | His 100 | Gly | Asp | Glu | Ser | Trp 105 | Gln | Glu | Tyr | Gln | Glu 110 | Phe | Leu |
| Gly | Leu | Pro 115 | Val | Ile | Lys | Arg | Leu 120 | Val | Phe | Pro | Lys | Asp 125 | Cys | Asn | Ile |
| Leu | Leu 130 | Ser | Ala | Ala | Ser | Gln 135 | Lys | Pro | His | Ser | Phe 140 | Ile | Pro | Leu | Phe |
| Asp 145 | Ser | Glu | Ala | Gly | Gly 150 | Thr | Gly | Glu | Leu | Leu 155 | Asp | Trp | Asn | Ser | Ile 160 |
| Ser | Asp | Trp | Val | Gly 165 | Arg | Gln | Glu | Ser | Pro 170 | Glu | Ser | Leu | His | Phe 175 | Met |
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| <211 | .> : | 111 | | | | | | | | | | | | | |
| <212 | ?> I | ONA | | | | | | | | | | | | | |
| <213 | 8 > 8 | Sacch | naron | nyces | cei | evis | siae | | | | | | | | |
| <400 gate | | L3 Eta g | gatta | aato | gg cg | gttat | tggt | gtt | gato | ıtaa | gcgg | gaggt | gt g | ggaga | ıcaaat |
| ggto | gtaaa | aag a | ctct | aaca | a aa | tago | caaat | tto | gtca | aaa | atgo | ctaag | jaa a | ı | |
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cctaaggagg atgttttggc tetggteaat gattaeggea ttgatategt ccaactgeac 300
ggagatgagt cgtggcaaga ataccaagag tteeteggtt tgccagttat taaaagaete 360
gtattteeaa aagaetgeaa catactaete agtgeagett cacagaaace teattegttt 420
atteeettgt ttgatteaga ageaggtggg acaggtgaac tttttggattg gaactegatt 480
tetgactggg ttggaaggea agagageee gagagettae attttatgtt agetggtgga 540
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Met Ser Val Ile Asn Phe Thr Cys Ser Ser Gly Pro Leu Val Lys Val 1 5 10 15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp 20 25 30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile 35 40 45

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys 50 55 60

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln 65 70 75 80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile 85 90 95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110 \hspace{1.5cm}$

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile \$115\$

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe 130 135 140 Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile 145 150 155 160 Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met 165 170 Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu 180 Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val 195 200 <210> 17 <211> 36 <212> DNA <213> Saccharomyces cerevisiae <220> <221> mutation <222> (1)..(1) <223> missing sequence before base 1 of SEQ17, corresponding to base 63 7 of wild-type: GAGACAAATGGTGTAAAAGACTCT <400> 17 aacaaaatag caaatttcgt caaaaatgct aagaaa 36 <210> 18 <211> 12 <212> PRT <213> Saccharomyces cerevisiae <400> 18 Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys

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<213> Artificial Sequence

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Glu Lys Glu Leu Gln Ala Gly Ser Gly Ser Gly

<210> 20

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<213> Artificial Sequence

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Lys Trp Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys Lys 20 25 30

Lys Leu Gln Ala Gly Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ala 35 40 45

Phe Leu

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| aattag | | 66 |
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| gtttt | | 65 |
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| ggcgga | torg gardaggege aaggaaaatt teaagtetrig | 40 |
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PBPF001W0 / 03.01.07 23 seq

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